

CLAIMS

1. A protein mass tag (PMT) reagent for mass spectrometric analysis of proteins comprised of an amino acid reactive moiety that selectively reacts with certain protein functional groups, wherein said protein mass tag is differentially labeled with one or more non-isotopic chemical substituents.

2. The PMT reagent of claim 1, wherein said non-isotopic chemical substituents are selected from the group consisting of homologous organic substituents and halides.

3. The PMT reagent of claim 1, wherein said amino acid reactive moiety reacts with certain protein functional groups via a covalent reaction.

4. The PMT reagent of claim 3, wherein said protein functional group is an amino acid side chain.

5. The PMT reagent of claim 3, wherein said protein functional group is a post-translationally modified amino acid side chain.

6. The PMT reagent of claim 1, wherein said protein functional group is selected from the group consisting of an amino acid, a modified amino acid, a post-translationally modified amino acid, a set of amino acids, a digested peptide or protein fragment.

7. The PMT reagent of claim 1, wherein said amino acid reactive moiety reacts with the guanidinium group of arginine.

8. A plurality of PMT reagents for mass spectrometric analysis of proteins each comprised of an amino acid reactive moiety that selectively reacts with certain protein functional groups, wherein each of said PMT reagents is differently labeled with one or more non-isotopic chemical substituents.

9. The PMT reagent of claim 8 wherein said non-isotopic chemical substituents are selected from the group consisting of homologous organic substituents and halides.

10. The PMT reagent of claim 8 wherein said protein reactive moieties react with certain protein functional groups via covalent reactions.

11. The PMT reagent of claim 8 wherein said protein reactive moiety reacts with the side chain of arginine.

12. A plurality of PMT reagents for mass spectrometric analysis of proteins having the general formula:

RM-PRM

wherein RM is a recognition moiety and PRM is an amino acid reactive moiety that selectively reacts with certain protein functional groups, wherein each of said PMT reagents is differentially labeled with one or more non-isotopic chemical substituents.

13. The PMT reagents of claim 12 wherein RM is selected from the group consisting of biotin or an oligonucleotide having between 5 and 50 bases.

14. The PMT reagents of claim 12, wherein said non-isotopic chemical substituents are selected from the group consisting of homologous organic substituents and halides.

15. The PMT reagent of claim 12, wherein said amino acid reactive moiety reacts with certain protein functional groups via a covalent reaction.

16. The PMT reagent of claim 12, wherein said amino acid reactive moiety reacts with the guanidinium group of arginine.

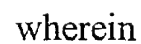
17. A plurality of PMT reagents for mass spectrometric analysis of proteins having the general formula:

RM-AM-PRM

wherein RM is a recognition moiety, AM is an accessory moiety and PRM is an amino acid reactive moiety that selectively reacts with certain protein functional groups, wherein each of said PMT reagents is differentially labeled with one or more non-isotopic chemical substituents.

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R is selected from the group consisting of an optionally substituted: C₁-C₂₀ alkyl, C₂-C₂₀ alkenyl, C₂-C₂₀ alkynyl, including deuterium substitutions; and

n = 0-10

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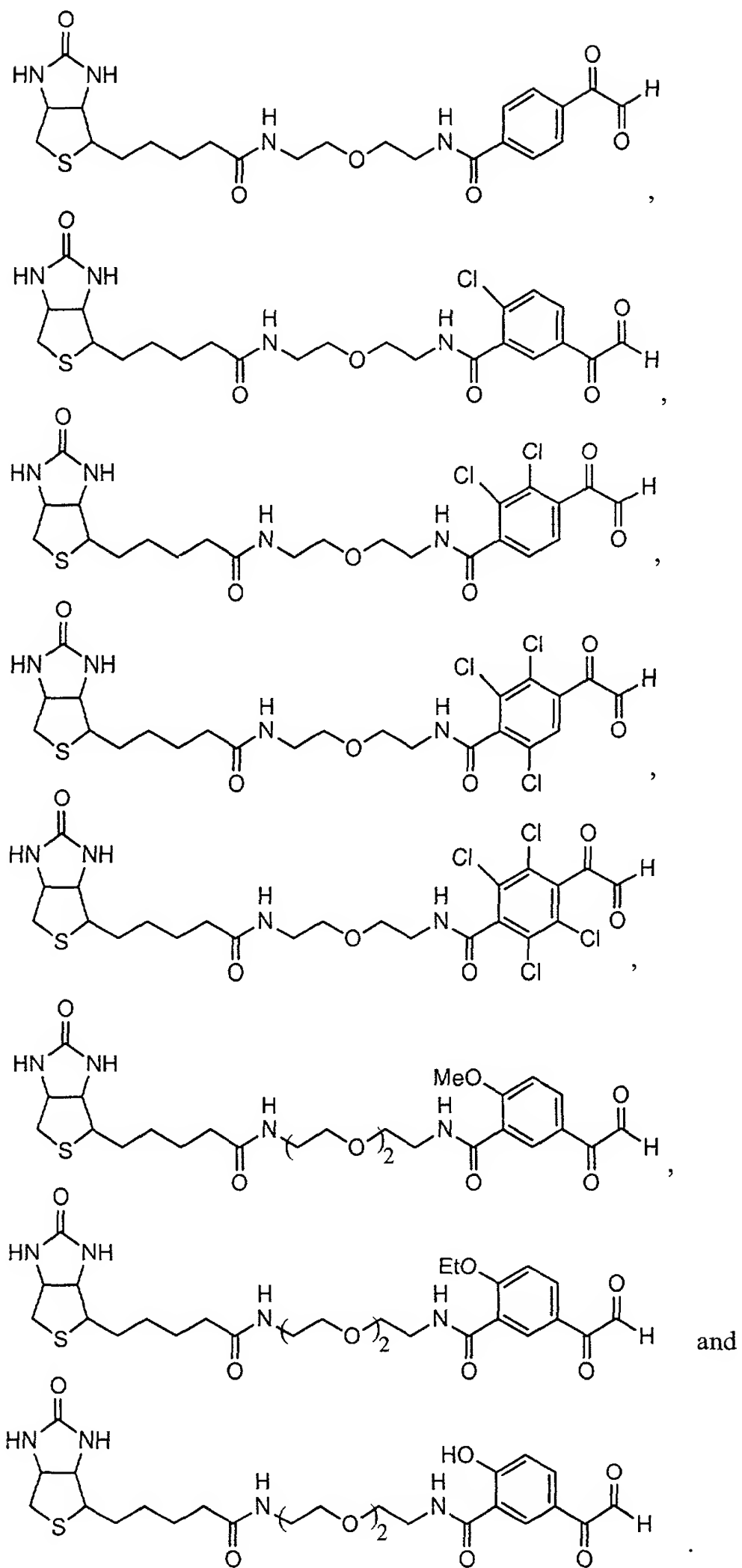
Chemical structures of compounds 1 and 2, which are thiazolidine-4-carboxamides. Both structures feature a thiazolidine-4-carboxamide moiety linked via a hexamethylene chain to a poly(ethylene glycol) (PEG) linker, which is further connected to a bis-benzoyl moiety. The bis-benzoyl moiety consists of two benzoyl groups linked by a central carbonyl group. The benzene rings of the bis-benzoyl moiety are substituted with 'X' groups. Structure 1 shows a specific substitution pattern, while structure 2 shows a different substitution pattern. The PEG linker is represented as $-(CH_2CH_2O)_n-$.

X is independently selected from the group consisting of H, D, OH, OD, R, OR, OSiR₃, Cl, Br, I, F, SH, SR, NH₂, NHR, and NR₂;

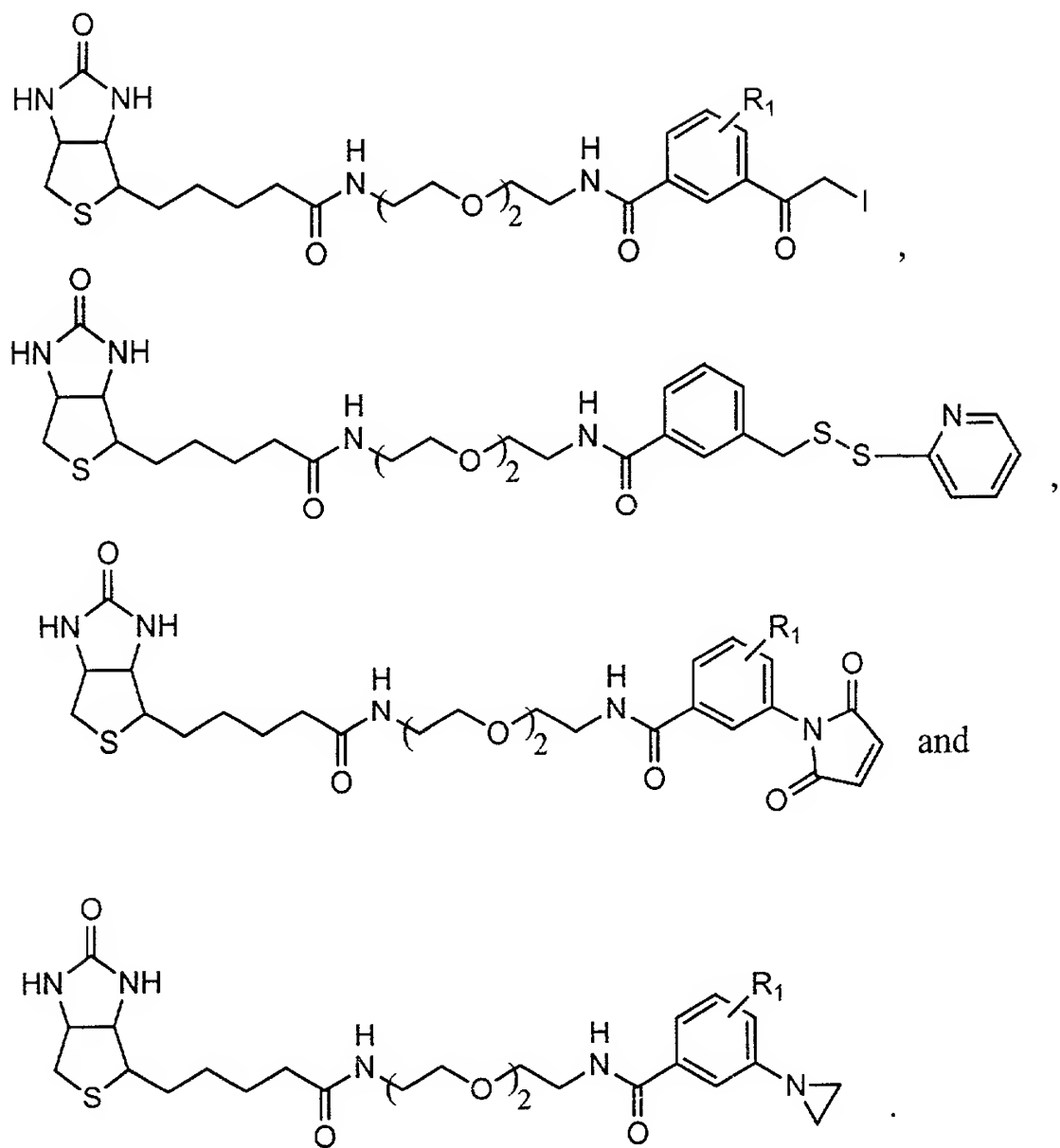
R is selected from the group consisting of an optionally substituted: C₁-C₂₀ alkyl, C₂-C₂₀ alkenyl, C₂-C₂₀ alkynyl, including deuterium substitutions; and

5 n = 0-10.

21. A compound having the following formula:



22. A compound having the formula:



5 23. A method for identifying one or more proteins or protein components in one or more samples containing a mixture of proteins or protein components comprising:

a) providing a plurality of PMT reagents wherein each PMT reagent is comprised of an amino acid reactive moiety that selectively reacts with certain protein functional groups, wherein each of said PMT reagents is differently labeled with one or more non-isotopic chemical substituents;

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- b) contacting each sample with one of the PMT reagents to produce proteins or protein components in each sample labeled with a different PMT reagent;
- c) isolating said labeled proteins or protein components; and
- d) analyzing said labeled proteins or protein components.

24. The method of claim 23, further comprising digesting the proteins or protein components after containing the sample with the PMT reagents.

5 25. The method of claim 24 wherein the labeled proteins or protein components are analyzed by mass spectrometry.

26. A method for comparing two or more samples containing a mixture of one or more proteins or protein components comprising:

10 a) providing a plurality of PMT reagents wherein each PMT reagent is comprised of an amino acid reactive moiety that selectively reacts with certain protein functional groups, wherein each of said PMT reagents is differently labeled with one or more non-isotopic chemical substituents;

b) contacting each sample with a different PMT reagent to produce proteins or protein components in each sample labeled with a different PMT reagent;

15 c) isolating said labeled proteins or protein components; and

d) simultaneously analyzing said labeled proteins or protein components to quantitatively determine the relative amounts of protein or protein components in each sample.

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